

1  
GTCCCTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTCTCTGTCTGCTCGCCGCTG  
-----+-----+-----+-----+-----+-----+-----+-----+  
CAGGAAGTGTGTAAGTACGACCGAAGAACAGAGACACCGCACAAAGAGACGAGCGCGGAC  
M H S L G F F S V A C S L L A A A  
60  
CGCTGCTCCCGGGTCTCGCGAGGCGCCGCGCGCGCGCGCGCTTCGAGTCCGGACTCG  
-----+-----+-----+-----+-----+-----+-----+-----+  
GCGACGAGGGCCAGGAGCGCTCCGCGGGCGGGCGGGCGGGAAGCTCAGGCCTGAGC  
L L P G P R E A P A A A A A F E S G L D  
120  
ACCTCTCGGACGGGAGCCCGACGCGGGCGAGGCCACGGCTTATGCAAGCAAGATCTGG  
-----+-----+-----+-----+-----+-----+-----+-----+  
TGGAGAGCCTGCGCCTCGGGCTGCGCCCGCTCCGGTGCCGGAATACGTTCTGTCTAGACC  
L S D A E P D A G E A T A Y A S K D L E  
180  
AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACCTCATGACTGTACTCTACCCAGAAT  
-----+-----+-----+-----+-----+-----+-----+-----+  
TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA  
E Q L R S V S V D E L M T V L Y P E Y  
240  
ATTGGAATAATGTACAAGTGTGCTAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG  
-----+-----+-----+-----+-----+-----+-----+-----+  
TAACCTTTTACATGTTACAGTCGATTCCCTTTCCTCCGACCGTGTATTGTCTCTTGTCC  
W K M Y K C Q L R K G G W Q H N R E Q A  
300  
CCAACCTCAACTCAAGGACAGAAAGAGACTATAAAATTGCTGCAGCACATTATAACAG  
-----+-----+-----+-----+-----+-----+-----+-----+  
GGTGGAGTTGAGTTCCTGCTCTCTGATATTTTAAACGACGTCGTGTAATATATGTC  
N L N S R T E E T I K F A A A H Y N T E  
360

FIG. 1A

MATCH WITH FIG. 1B



MATCH WITH FIG. 1A

361 AGATCTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT  
-----+-----+-----+-----+-----+-----+-----+  
TCTAGAACTTTTCATAAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA  
I L K S I D N E W R K T Q C M P R E V C  
420

421 GTATAGATGTGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCAATGTG  
-----+-----+-----+-----+-----+-----+-----+  
CATATCTACACCCCTTCCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC  
I D V G K E F G V A T N T F F K P P C V  
480

481 TGTCCGCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA  
-----+-----+-----+-----+-----+-----+-----+  
ACAGGCAGATGTCTACACCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT  
S V Y R C G G C C N S E G L Q C M N T S  
540

541 GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCA  
-----+-----+-----+-----+-----+-----+-----+  
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTACGGAGAGAGAGTTCCGGGT  
T S Y L S K T L F E I T V P L S Q G P K  
600

601 AACCAGTAACAATCAGTTTGGCCAAATCACACTTCCTGCCGATGCATGCTAAACTGGATG  
-----+-----+-----+-----+-----+-----+-----+  
TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTAC  
P V T I S F A N H T S C R C M S K L D V  
660



MATCH WITH FIG. 1B

661 TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC  
-----+-----+-----+-----+-----+  
AAATGTCTGTCAAGTAAGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTACACAG  
Y R Q V H S I I R R S L P A T L P Q C Q  
720

721 AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC  
-----+-----+-----+-----+-----+  
TCCGTGCGCTTGTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCCTACGG  
A A N K T C P T N Y M W N N H I C R C L  
780

781 TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC  
-----+-----+-----+-----+-----+  
ACCGAGTCCTTCTAAATAACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG  
A Q E D F M F S S D A G D D S T D G F H  
840

841 ATGACATCTGTGGACCAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG  
-----+-----+-----+-----+-----+  
TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCAACAGACGTCCTC  
D I C G P N K E L D E E T C Q C V C R A  
900

901 CGGGGCTTCGGCCTGCCAGCTGTGGACCCCAAGAACTAGACAGAACTCATGCCAGT  
-----+-----+-----+-----+-----+  
GCCCCGAAGCCGACGGTCGACACCTGGGGTGTCTTCTGATCTGTCTTTGAGTACGGTCA  
G L R P A S C G P H K E L D R N S C Q C  
960

FIG. 1C

MATCH WITH FIG. 1D

MATCH WITH FIG. 1C

961	GTGTCTGTAAAAA	CTCTCC	CAGCCAATGTGGG	CCCAACCGAGAATTTGATGAAA	1020
	-----+	-----+	-----+	-----+	
	CACAGACATTTT	TGTGAGAAGGGT	CGGTACACCCCGT	TGGCTCTTAAAC	TACTTT
	V C K N K L F P S Q C G A N R E F D E N				
	ACACATGCCAGTGTGTA	GTAAAAAGAACCTG	CCCCAGAAATCAACCCCTAAATCCTGGAA		1080
	-----+	-----+	-----+	-----+	
	TGTGTACGGTCA	CACATACATTTCTTGGACGGGTCTT	AGTTGGGATTTAGGACCTT		
	T C Q C V C K R T C P R N Q P L N P G K				
	AATGTGCCCTGTGAATGTACAGAAAAGTCCACAGAAATGCTTGT	TAAAAAGAAAGTTCC			1140
	-----+	-----+	-----+	-----+	
	TTACACGGACACTTACATGTC	TTTCAGGTGCTTTACGAACAATTTCCCTTCTTCAAGG			
	C A C E C T E S P Q K C L L K G K K F H				
	ACCACCAAACATGCAGCTGTTACAGACGGCCCATGTACGAACCGCCAGAAAGGCTTGTGAGC				1200
	-----+	-----+	-----+	-----+	
	TGGTGGTTTGTACGTCGACAATGTC	TGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG			
	H Q T C S C Y R R P C T N R Q K A C E P				
	CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATAT	TGGCAAGACCAC			1260
	-----+	-----+	-----+	-----+	
	GTCCTAAAAAGTATATCACTTCTT	CACAGCAACACAGGGAAGTATAACCGTTTCTGGTG			
	G F S Y S E E V C R C V P S Y W Q R P Q				

FIG. 1D

MATCH WITH FIG. 1E



## MATCH WITH FIG. 1D

1261	AAATGAGCTAAGATTGTACTGTTTCCAGTTTCATCGATTTTCTATTATGGAACAACTGTGT -----+-----+-----+-----+-----+-----+-----+-----+ TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA M S *	1320
1321	TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCCTTGTGGGTCCATGCTAACAAAAGACA -----+-----+-----+-----+-----+-----+-----+-----+ ACGGTGTCACTTGACAGACACTTGTCTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT -----+-----+-----+-----+-----+-----+-----+-----+ AAAGTCTGTCTTCCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG -----+-----+-----+-----+-----+-----+-----+-----+ TTTCAGACAGAAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC -----+-----+-----+-----+-----+-----+-----+-----+ CAAAAGGCCCTCTTGTAAAGACTGGTTTCTTGCCAAATGACCCAAACAGCCCAAGATTTTCCTC -----+-----+-----+-----+-----+-----+-----+-----+ GTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCTGGTTCTAAAAGGAG -----+-----+-----+-----+-----+-----+-----+-----+ TTGTGATTTCTTTAAAGAAATGACTATATAATTATTATTTCCACTAAAAATATTGTTTCTGTC -----+-----+-----+-----+-----+-----+-----+-----+ AACACTAAAGAAAATTTCTTACTGATATATTAATAAAGGTGATTTTATAACAAAAGACG -----+-----+-----+-----+-----+-----+-----+-----+ ATTCAATTTTATAGCAACAACAATTGGTAAACCTCACTGTGATCAATATTTTATATCAT -----+-----+-----+-----+-----+-----+-----+-----+ TAAGTAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAAATATAGTA -----+-----+-----+-----+-----+-----+-----+-----+ GCAAAATATGTTTAAATATAAATGAAAATTGTATTTTATAAAAAAATAAAAAA -----+-----+-----+-----+-----+-----+-----+-----+ CGTTTATACAAAATTTTATTTTACTTTTAAACATAAAATATTTTTTTTTTTTTTT	1380
1381		1440
1441		1500
1501		1560
1561		1620
1621		1674

FIG. 1E

1 CGAGGCCACGGCTTATGCAAGCAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT  
-----+-----+-----+-----+-----+-----+-----+-----+  
61 AGATGAACTCATGACTGTACTCTACCCAGAATATGGAAAAATGTACAAGTGTCAAGCTAAG  
-----+-----+-----+-----+-----+-----+-----+-----+  
M T V L Y P E Y W K M Y K C Q L R  
121 GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC  
-----+-----+-----+-----+-----+-----+-----+-----+  
K G G W Q H N R E Q A N L N S R T E E T  
181 TATAAAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG  
-----+-----+-----+-----+-----+-----+-----+-----+  
I K F A A A H Y N T E I L K S I D N E W  
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGCAGTTTGGAGT  
-----+-----+-----+-----+-----+-----+-----+-----+  
R K T Q C M P R E V C I D V G K E F G V  
301 CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCTG  
-----+-----+-----+-----+-----+-----+-----+-----+  
A T N T F F K P P C V S V Y R C G G C C

MATCH WITH FIG. 2B

FIG. 2A

MATCH WITH FIG. 2A

421 TGA A A T T A C A G T G C C T C T C T C A A G G C C C C A A A C C A G T A A C A A T C A G T T T G C C A A T C A  
E I T V P L S Q G P K P V T I S F A N H

481 C A C T T C C T G C C G A T G C A T G T T A A A C T G G A T G T T T A C A G A C A A G T T C A T T C C A T T A T T A G  
T S C R C M S K L D V Y R Q V H S I I R

541 A C G T T C C C T G C C A G C A A C A C T A C C A C A G T G T C A G G C A G C G A A C A A G A C C T G C C C C A C C A A  
R S L P A T L P Q C Q A A N K T C P T N

601 T T A C A T G T G G A A T A A T C A C A T C T G C A G A T G C C T G G C T C A G G A A G A T T T A T G T T T C C T C  
Y M W N N H I C R C L A Q E D F M F S S

661 G G A T G C T G G A G A T G A C T C A A C A G A T G G A T T C C A T G A C A T C T G T G G A C C A A A C A A G G A G C T  
D A G D D S T D G F H D I C G P N K E L

721 G G A T G A G A G A C C T G T C A G T G T G T C T G C A G A G C G G G C T T C G C C T G C C A G C T G T G G A C C  
D E E T C Q C V C R A G L R P A S C G P

MATCH WITH FIG. 2C

FIG. 2B

**MATCH WITH FIG. 2B**

[illegible]

**MATCH WITH FIG. 2D**

**FIG. 2C**



**MATCH WITH FIG. 2C**

1141 GTTCATCGATTTTCTATTATGGAAAACCTGTGTTGCCACAGTAGAACTGTCTGTGAACAGA  
-----+-----+-----+-----+-----+-----+-----+-----+  
1201 GAGACCCCTGTGGGTCCATGCTAACAAAGACACAAAAGTCTGTCTTTTCCTGAACCATGTGGA  
-----+-----+-----+-----+-----+-----+-----+-----+  
1261 TAACTTTACAGAAAATGGACTGGAGCTCATCTGCAAAAGGCCCTCTTGTAAAGACTGGTTTT  
-----+-----+-----+-----+-----+-----+-----+-----+  
1321 CTGCCAATGACCAACAGCCCAAGATTTTCCCTCTTGTGATTTTCTTTAAAAAGAAATGACTATA  
-----+-----+-----+-----+-----+-----+-----+-----+  
1381 TAAATTTATTTCCCACTAAAAATATTGTTTCTGTCATTCATTTTATAGCAACAACAATGGT  
-----+-----+-----+-----+-----+-----+-----+-----+  
1441 AAAACTCACTGTGATCAATATTTTATATCATGCAAAATATGTTTAAAAATAAAATGAAAA  
-----+-----+-----+-----+-----+-----+-----+-----+  
1501 TTGTATTATAAAAAAAAAAAAAAA  
-----+-----+-----+-----+-----+-----+-----+-----+

**FIG. 2D**

1		50
Pdgfa	.MRTLACLLL LCCYLALVL AEEAIPREV IERLARQIH SIRDQLRLE	
Pdgfb	MNRCAW.LFL SLCCYLRLVS AEGDPIPEEL YEMLSOHSIR SFDDLQRLH	
Vegf	.....MNFL SWHWSLALL LY.....LHHAKWSOA	
Vegf2	.....MTV LYPEYKMYK CQ.....LRKGGWQH	
51		100
Pdgfa	IDSVGSEDSL DISLRAHGVH ATKHVPEKRP LPIRRKRSI.....EEAVP	
Pdgfb	GDP.GEEDGA ELDLNMTRSH SGGELES...LARGRRSLG SLTIAEPAMI	
Vegf	APMAE.....GGCQ NHHEVVKFMD.VYQR.....	
Vegf2	REQANLSRT EETIKFAAH YNTEILKSID NEWRK.....	
101		150
Pdgfa	AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCCTGCC NTSSVKQOPS	
Pdgfb	AECKTRTEVF EISRRLLDRT NANFLVWPPC VEVQRCSCCC NNRNVQCRPT	
Vegf	SYCHPIETLV DIFQEYPDEI..EYIFKPS VPLMRGCGCC NDEGLECVPT	
Vegf2	TQCMPREVCI DVGKEFGVAT..NTFFKPPC VSVYRCGCGCC NSEGLQCMNT	
151		200
Pdgfa	RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLEQAC.....AT.....	
Pdgfb	QVQLRPVQVR KIEIVRKKPI FKKAIVTLED HLACQ.....ETVAAARPVT	
Vegf	EESNITMQIM RIK.PH..QC QHIGEMSFLO HNKCELRPKK DRARQEKKSV	
Vegf2	STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSQRMMSKL DVYROVHSII	

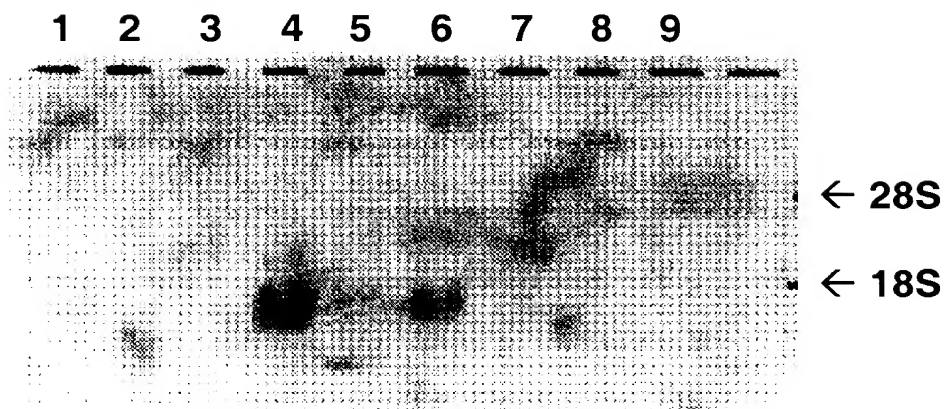
FIG. 3A

201		250
Pdgfa	..... TSLNPD YREEDTDVR	
Pdgfb	RSPGGSOEQR AKTPQTRVTI	RTVVRVRPPK GKHFKKHTH DK TALKETLG
Vegf	RGK.....	CKGQKRKRK KSRYSWSVY VGARCCCLMPW SLP GPH
Vegf2	RRSLPATLPQ COAANKTCPT	NYMNNHICR CLAQEDFMFS SDAGDDSDTG
251		300
Pdgfa	.....	
Pdgfb	A.....	
Vegf	..... CCGP	CSE RRKHLFVQDP QTKCSCSKNT
Vegf2	FHDICGNKE LDEETCCVC	RAGLRPASC G PHKEL... DR NSCQCVCCKNK
301		350
Pdgfa	.....	
Pdgfb	.....	
Vegf	DSRCKARQ LELNERTCRC DKPRR	
Vegf2	LFPSQCCANR EFDENTCQC	VCKRTCPRNQ PLNPGKCACE CTESPOKCLL
351		398
Pdgfa	.....	
Pdgfb	.....	
Vegf	.....	
Vegf2	KGKKFHHQTC SCYRRPCTNR	QKACEPGFSY SEEVCRCPVS YWQRPQMS

FIG. 3B



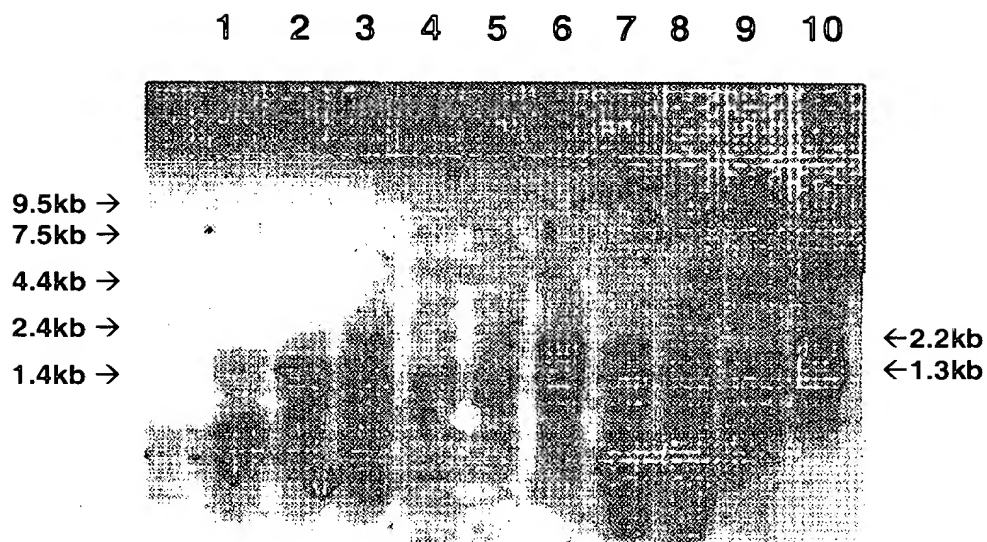
# Expression of VEGF2 mRNA in Human Breast Tumor Cells



Lane 1	Normal Tissue
Lane 2	Breast Tumor Tissue
Lanes 3-9	Breast Tumor Cell Lines

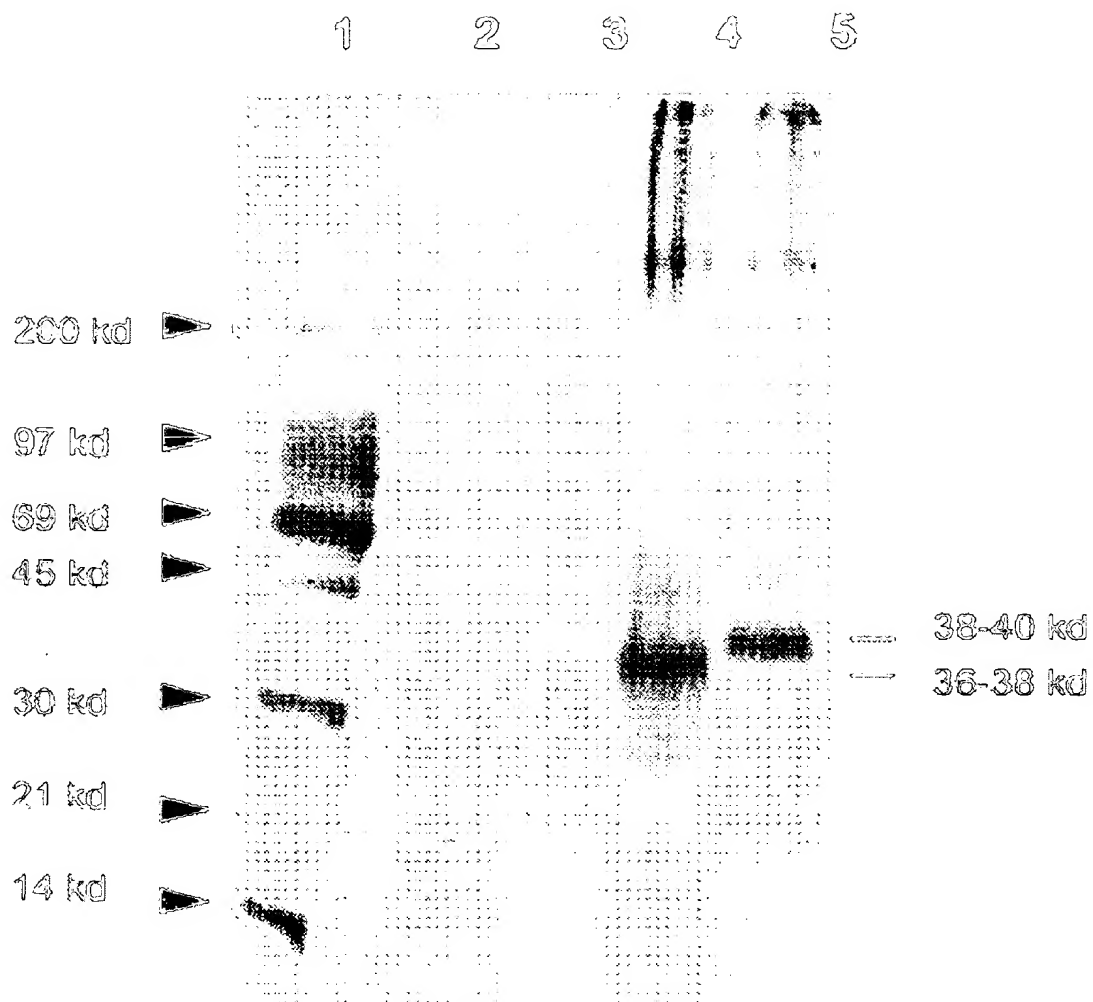
**FIG. 5**

# Expression of VEGF2 mRNA in Human Adult Tissues



- |                |                |
|----------------|----------------|
| 1. Ovary       | 6. Lung        |
| 2. Testes      | 7. Spleen      |
| 3. Gall Blader | 8. Prostate    |
| 4. Kidney      | 9. Hippocampus |
| 5. Liver       | 10. Heart      |

FIG. 6



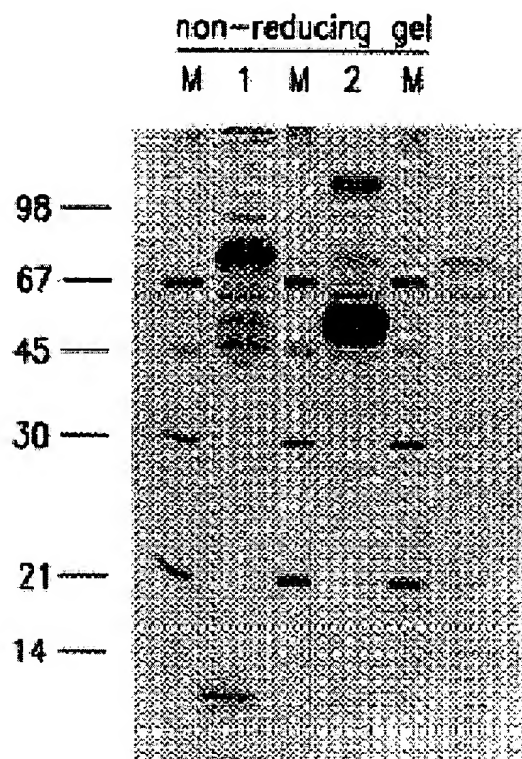
- Lane 1: 14-C and rainbow M.W. marker
- Lane 2: FGF control
- Lane 3: VEGF2 (M13-reverse & forward primer)
- Lane 4: VEGF2 (M13-reverse & VEGF-F4 primer)
- Lane 5: VEGF2 (M13-reverse & VEGF-F5 primer)

FIG. 7



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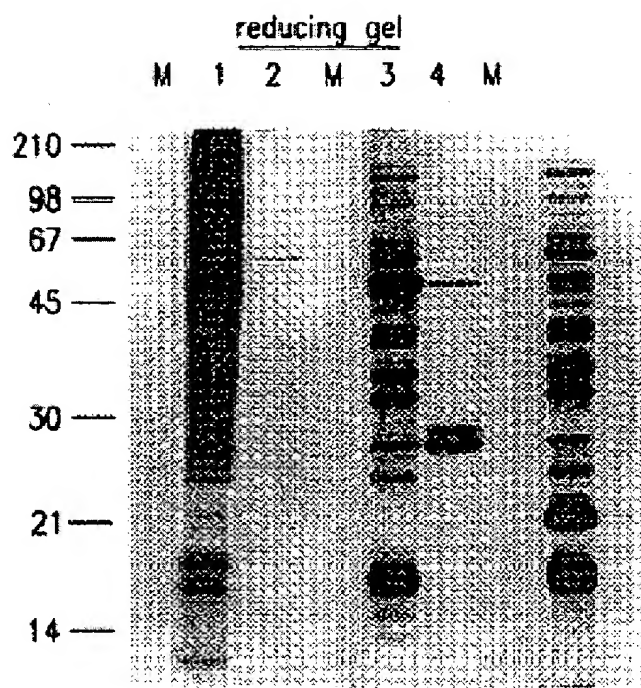
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TECH CENTER 1600/2900



Lane M: Marker  
Lane 1: Vector medium  
Lane 2: VEGF2 medium

FIG. 8A





Lane M: Marker  
Lane 1: vector cytoplasm  
Lane 2: vector medium  
Lane 3: VEGF2 cytoplasm  
Lane 4: VEGF2 medium

**FIG. 8B**

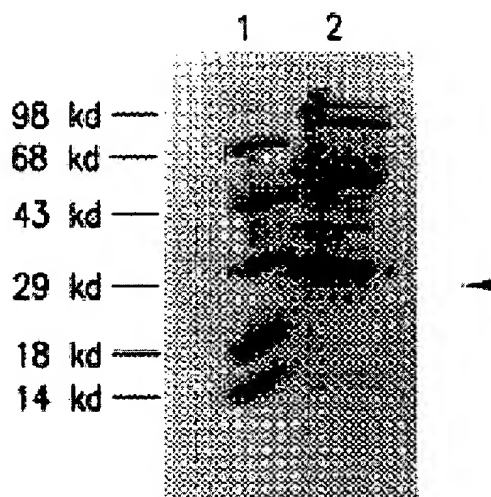


FIG. 9

Lane 1: Molecular weight marker  
Lane 2: Precipitates containing VEGF2.

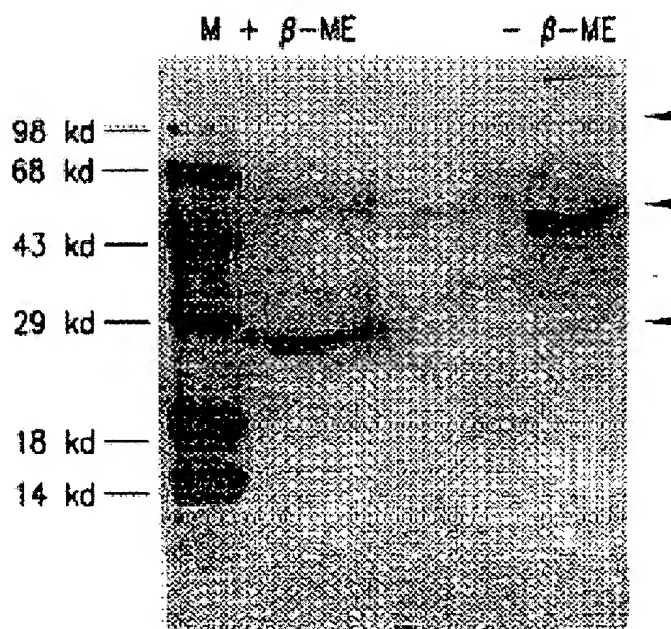


FIG. 10



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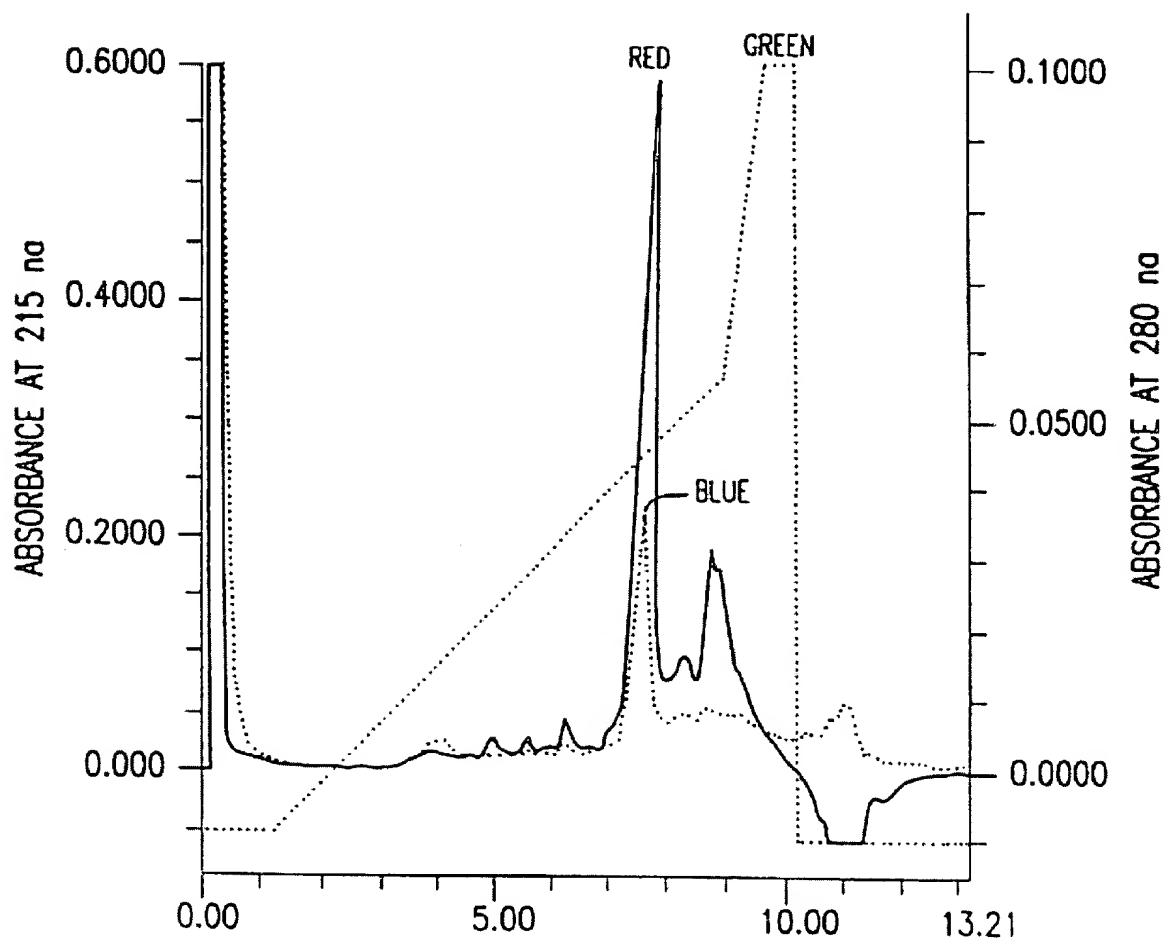


FIG. 11

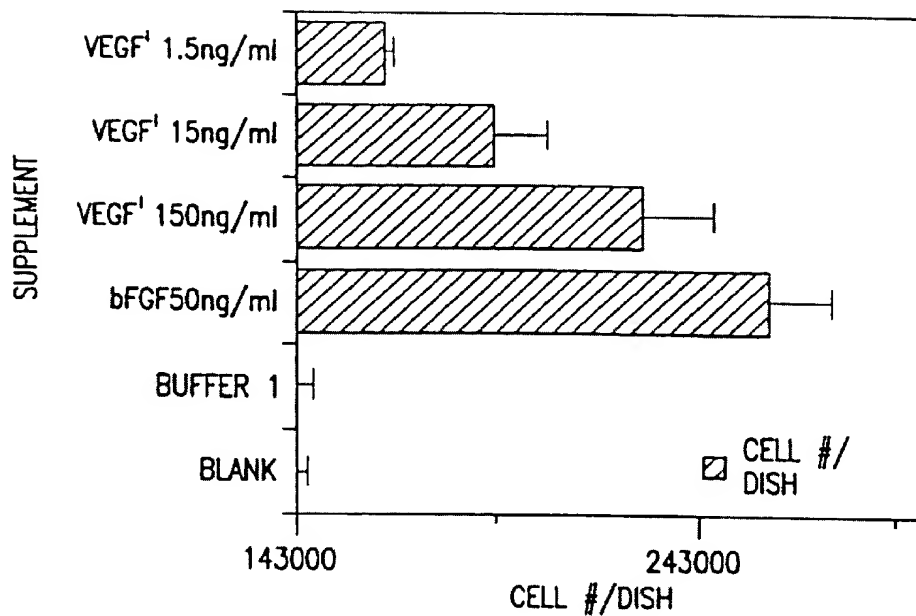


FIG. 12

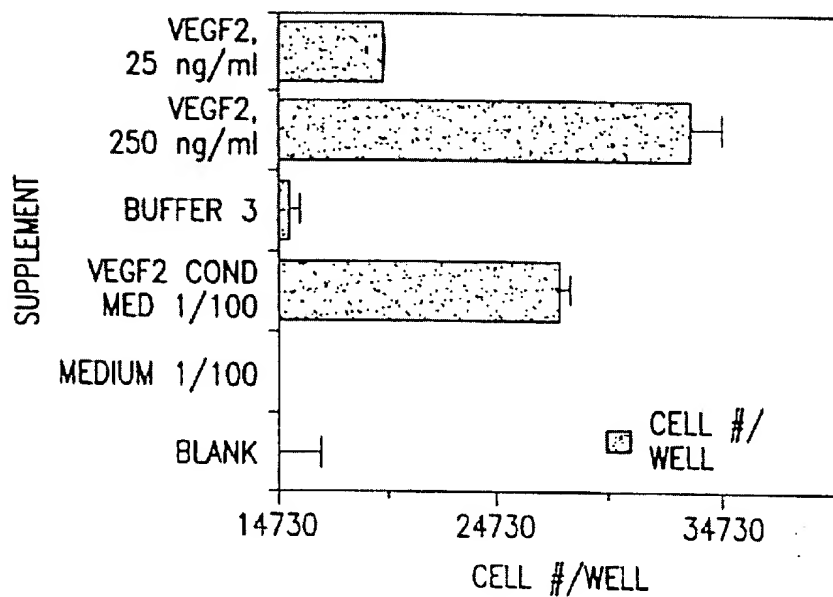


FIG. 13